Protein Molecular Spectral Features in Hull-less Barley Varieties and Their Relation to Protein and Energy Values

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Key Words: barley, infrared spectroscopy, protein molecular structure, protein value

Abstract

The objectives of this study were to investigate the relationship between the protein molecular spectral features and protein and energy values in dairy cows of four hull-less barley (HB) varieties (normal starch conventional - CDC McGwire; zero-amylose waxy- CDC Fibar, waxy – CDC Rattan, and high-amylose – HB08302) using diffuse reflectance infrared fourier transform spectroscopy. The items included IR absorbed intensity (IR intensity unit, KM) peak area attributed to protein amide I (ca. 1715-1575 cm^{-1}), amide II (ca. 1575-1490 cm^{-1}), and ratio of amide I to II. The results show that (1) zero-amylose waxy was the greatest in protein amide I and II infrared reflectance peak areas; (2) α-helix to β-sheet ratio differed among HB: high-amylose was the greatest, zero-amylose waxy and waxy were the intermediate, and normal starch was the lowest; (3) altered starch (CDC Fibar, CDC Rattan, and HB08302) HB varieties were similar to each other, but were different from normal starch variety in protein structural makeup; and (4) the rate and extent of rumen degradation of starch and protein were highly related to the molecular structural makeup of HB. In conclusion, this study indicated that (1) protein molecular structure affects metabolic characteristics of the proteins of HB, and (2) the altered starch HB seem to be more favorable to ruminants in terms of protein and energy values.

Introduction

Barley is (*Hordeum vulgare* L.) the fourth largest cereal crop produced in the world. Canada is among the top five barley producers and exporters in the world with the annual barley production close to 12 million tonnes (FAOSTAT, 2008). Canada has locally adapted and registered 200 varieties of barley. There are over 50 barley varieties produced in western Canada, including 8 hull-less types, 13 malting types, and some others suitable for livestock industry. Recently, several new Canadian barley varieties, including hull-less waxy genotypes such as CDC Fibar, and CDC Rattan, as well as a high amylose line HB08302 have been developed, specifically for food use. Although these HB are developed for food, fluctuations in crop industry will allow some crops to be used for multiple purposes rather than for single purpose. For instance, if (a) high economic opportunity for barley occurs and its market price goes down; then food barley may become a better alternative for livestock producers as animal feed; or (b) the barley does not meet food standards because of lower quality of the grain due to environmental, mechanical, storage, and other factors; then it could be better utilized also, as animal feed.

The objectives of this study were to investigate the relationship between the protein molecular spectral features and protein and energy values in dairy cows of four hull-less barley varieties (normal starch conventional - CDC McGwire; zero-amylose waxy- CDC Fibar, waxy – CDC Rattan, and high-amylose – HB08302).

Materials and Methods

Four hull-less barley varieties: (1) CDC McGwire, (2) CDC Fibar, (3) CDC Rattan, and (4) HB08302 were chosen. Spectra from samples of these varieties were obtained using a FTS-40 Fourier transform vibrational infrared spectroscopy. The parameters assessed included (i) protein amide I, (ii) protein amide II, (iii) amide I to amide II ratio; (iv) their correlation to (a) starch, (b) protein rumen degradation kinetics, and (c) protein metabolic characteristics. Rumen degradation kinetics of CP were determined according to Ørskov and McDonald (1997) and starch degradation kinetics and potential nutrient supply were determined according to Tamminga et al. (1994).

Results and Discussion

Hull-less barley CDC Fibar had the largest ($P < 0.05$) protein amide I and II peak area among the varieties, indicating higher concentration of protein in this variety. While the amide I and II ratios for the newer barley varieties were similar ($P > 0.05$) to each other, they were lower (5.3, 5.5, and 4.9, CDC Fibar, CDC Rattan, and HB08302, respectively, $P < 0.05$) than the conventional variety (11.7), indicating that the newer varieties had similar protein profiles, which was different than the conventional feed-type barley variety. The correlation analysis showed the decreasing protein amide I to amide II ratio with decreasing rate of starch degradability ($r = 0.92$, $P = 0.01$) in the rumen and declining degraded protein balance ($r = - 0.72$, $P = 0.045$). Usually, barley starch sources that are less rapidly degraded in the rumen are preferable for ruminant feed because they are less likely to cause an accumulation of acidic fermentation products, which is detrimental to the rumen function. Hence, the results of the present study indicated that altered starch HB seem to be more favorable to ruminants by the magnitude of the amide I to amide II ratio than normal starch HB. All of four HB contained both α-helix and β-sheet. Results of the current study also revealed, that these HB differed in protein secondary structure conformation in terms of the α-helix and β-sheet and their ratio, indicating that the alteration of starch of barley through breeding using pedigree breeding system does not only change the grain protein amide I to amide II ratio, but it further affects the ratio of α-helix to β-sheet within the protein amide I of molecular structural makeup. Ratio of α-helix to β-sheet was correlated negatively with the rate of starch degradation ($r = - 0.75$, $P = 0.032$) and truly absorbed protein in the small intestine ($r = -0.76$, $P = 0.03$), suggesting that protein secondary structure differences among barley varieties may have an impact on protein utilization and availability in the rumen and the intestine in dairy cows. In conclusion, this study demonstrated that (1) protein molecular structure affects metabolic characteristics of the proteins of HB, and (2) the altered starch HB seem to be more favorable to ruminants in terms of protein and energy values.

Acknowledgments

We are grateful to Dr. Brian Rossnagel and Dr. Aaron Beattie - Crop Development Centre, the University of Saskatchewan (Saskatoon, Canada) for providing us barley samples. The authors also thank Ken Thoms, (Saskatchewan Structural Sciences Centre, University of Saskatchewan) and Zhiyuan Niu (Department of Animal and Poultry Sciences, University of Saskatchewan) for their support during laboratory analysis. This research has been supported by grant Saskatchewan Agricultural Development Fund and Ministry of Agriculture Strategic Research Chair fund.

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